American Journal of Hematology 60:173 (1999)

CORRIGENDUM

Ko T-M, Tseng L-H, Kao C-H, Lin Y-W, Hwa H-L, Hsu P-M, Li S-F, Chuang S-M. Molecular characterization and PCR diagnosis of Thailand deletion of α-globin gene cluster. Am J Hematol 1998;124–130.

Drs. Ko and Li have amended their figure originally published in the article referenced above, which is now being published here as Figure 1. They agree with Drs. Chong and Higgs in that they had mistakenly classified $--^{FIL}$ rather than $--^{THAI}$ in their earlier publication.

Editor

Molecular Characterization of the $--^{FIL}$ Determinant of Alpha-Thalassemia

Alpha-thalassemia is a common single gene disease worldwide [1]. In Taiwan, $--^{SEA}$ accounts for most alleles of α-thalassemia 1; however, more extensive deletions involving the ζ2-globin gene, $--^{FIL}$ and $--^{THAI}$, have also been reported [2,3]. To detect these alleles, we digested genomic DNA with *Hind*III and *Sst*I respectively and hybridized the blots with L0 probe [3]. Based on the fragment length of junction bands, we classified our carriers as having ''$--^{THAI}$'' and reported that this mutation was the second most common α-thalassemia 1 allele in Taiwan [3]. Recently, we have characterized the exact breakpoints of ''$--^{THAI}$'' and developed a gap-polymerase chain reaction (PCR) strategy for rapid diagnosis that uses primers T91 and T82 [4]. The defined breakpoints were different from those previously postulated by Fischel-Ghodsian et al. in 1988 [2,4].

Although Dr. Higgs and Dr. Chong could not amplify the expected 560 base-pair fragment from $--^{THAI}$ carriers using primers T91 and T82, they were able to amplify the expected fragment from $--^{FIL}$ carriers. Direct sequencing results of the amplified 560 base-pair product from $--^{FIL}$ carriers diagnosed by Dr. Chong matched those from our patients with ''$--^{THAI}$'' [4]. Dr. Chong and Dr. Higgs questioned if we mistakenly classified $--^{FIL}$ as $--^{THAI}$.

To answer this question, we reexamined the process of our characterization of ''$--^{THAI}$'' alleles and found that the fragment sizes of junction bands generated from *Hind*III and *Sst*I digestion of genomic DNA in carriers of $--^{THAI}$ and $--^{FIL}$ are quite similar. Differentiation bewteen $--^{THIA}$ and $--^{FIL}$ could have been achieved using Southern blot hybridization on *Eco*RI digested DNA [2,3].

According to the report by Fischel-Ghosdian et al. [2], the *Eco*RI site at coordinate −1 and the *Bgl*II site at −1.5 (with the initiator codon of the ζ2-globin gene as at coordinate 0) should be absent in the postulated $--^{THAI}$ allele. However, these two sites were present in our carriers with ''$--^{THAI}$'' alleles (Fig. 1). The defined breakpoints lay within the postulated region for $--^{FIL}$ rather than $--^{THAI}$ as originally reported [2,4]. After reanalysis of data from our study and the study of Dr. Higgs et al., we agree that we have mistakenly classified $--^{FIL}$ as $--^{THAI}$ and the breakpoints we had defined are really of $--^{FIL}$ rather than $--^{THAI}$. Figure 1 in our original report [reference 4] should thus be amended (Fig. 1).

In a yet to be published report, we found that about 2% of Filipinos were carriers of $--^{FIL}$ [5]. Correct classification and a rapid PCR diagnosis of this common α-thalassemia 1 allele is important in genetic counseling and prenatal diagnosis to prevent birth of Hb Bart's hydrops fetalis.

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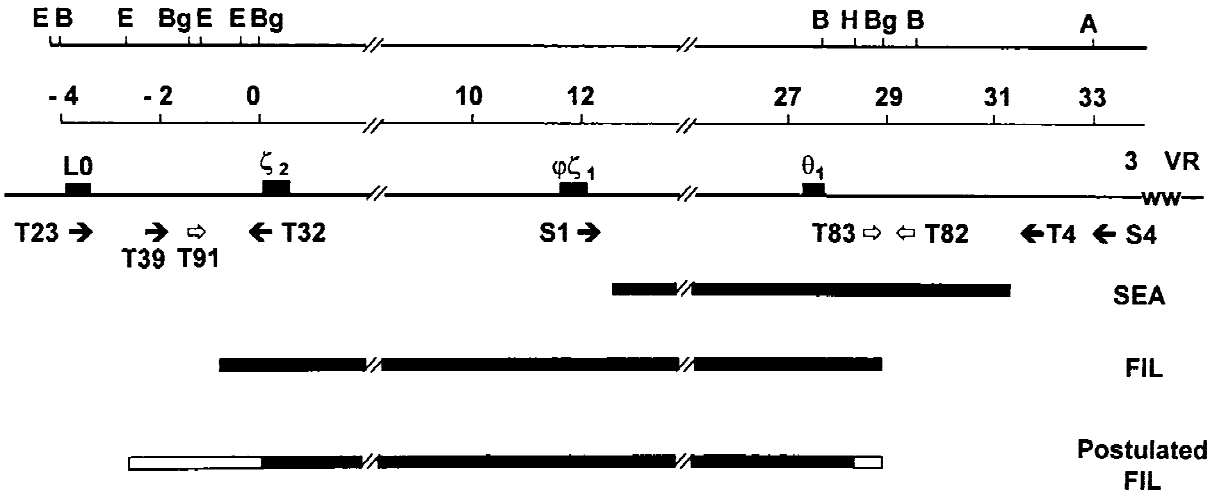

Fig. 1. Deletion extent of $--^{SEA}$, postulated and characterized extents of $--^{FIL}$. Coordinates are given in kb: 0 represents the initiator codon adenine of the ζ2-globin gene. B, *Bam*HI, Bg, *Bgl*II, E, *Eco*RI, H, *Hind*III, A, *Acc*I. Black bars indicate the deleted region and white bars indicate the segments within which the breakpoints lie. Black arrows indicate the primers used for DNA amplification and sequencing. White arrows indicate the primers used for DNA amplification across the $--^{FIL}$ and its corresponding normal sequence. 3 VR, 3′ hypervariable region.